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 ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150  
 ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200  
 TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250  
 TTCAAAAAC TCAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300  
 ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350  
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TAAAACTCTA	AACTTGACTA	AATACAGAGG	ACTGGTAATT	GTACAGTTCT	1850
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GTGTAAAAAT	CTGTAATACA	AATTTTTTAA	CTGATGCTTC	ATTTTGCTAC	1950
AAAATAATTT	GGAGTAAATG	TTTGATATGA	TTTATTTATG	AAACCTAATG	2000
AAGCAGAAAT	AAATACTGTA	TTAAAATAAG	TTCGCTGTCT	TT	2042

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Ser	Ser	Arg	Ile	Asp 20	Gln	Asp	Asn	Ser	Ser 25	Phe	Asp	Ser	Leu	Ser 30
Pro	Glu	Pro	Lys	Ser 35	Arg	Phe	Ala	Met	Leu 40	Asp	Asp	Val	Lys	Ile 45
Leu	Ala	Asn	Gly	Leu 50	Leu	Gln	Leu	Gly	His 55	Gly	Leu	Lys	Asp	Phe 60
Val	His	Lys	Thr	Lys 65	Gly	Gln	Ile	Asn	Asp 70	Ile	Phe	Gln	Lys	Leu 75
Asn	Ile	Phe	Asp	Gln 80	Ser	Phe	Tyr	Asp	Leu 85	Ser	Leu	Gln	Thr	Ser 90
Glu	Ile	Lys	Glu	Glu 95	Glu	Lys	Glu	Leu	Arg 100	Arg	Thr	Thr	Tyr	Lys 105
Leu	Gln	Val	Lys	Asn 110	Glu	Glu	Val	Lys	Asn 115	Met	Ser	Leu	Glu	Leu 120
Asn	Ser	Lys	Leu	Glu 125	Ser	Leu	Leu	Glu	Glu 130	Lys	Ile	Leu	Leu	Gln 135
Gln	Lys	Val	Lys	Tyr 140	Leu	Glu	Glu	Gln	Leu 145	Thr	Asn	Leu	Ile	Gln 150
Asn	Gln	Pro	Glu	Thr 155	Pro	Glu	His	Pro	Glu 160	Val	Thr	Ser	Leu	Lys 165
Thr	Phe	Val	Glu	Lys 170	Gln	Asp	Asn	Ser	Ile 175	Lys	Asp	Leu	Leu	Gln 180
Thr	Val	Glu	Asp	Gln 185	Tyr	Lys	Gln	Leu	Asn 190	Gln	Gln	His	Ser	Gln 195
Ile	Lys	Glu	Ile	Glu 200	Asn	Gln	Leu	Arg	Arg 205	Thr	Ser	Ile	Gln	Glu 210
Pro	Thr	Glu	Ile	Ser 215	Leu	Ser	Ser	Lys	Pro 220	Arg	Ala	Pro	Arg	Thr 225
Thr	Pro	Phe	Leu	Gln 230	Leu	Asn	Glu	Ile	Arg 235	Asn	Val	Lys	His	Asp 240
Gly	Ile	Pro	Ala	Glu 245	Cys	Thr	Thr	Ile	Tyr 250	Asn	Arg	Gly	Glu	His 255
Thr	Ser	Gly	Met	Tyr 260	Ala	Ile	Arg	Pro	Ser 265	Asn	Ser	Gln	Val	Phe 270
His	Val	Tyr	Cys	Asp 275	Val	Ile	Ser	Gly	Ser 280	Pro	Trp	Thr	Leu	Ile 285

Gln	His	Arg	Ile	Asp 290	Gly	Ser	Gln	Asn	Phe 295	Asn	Glu	Thr	Trp	Glu 300
Asn	Tyr	Lys	Tyr	Gly 305	Phe	Gly	Arg	Leu	Asp 310	Gly	Glu	Phe	Trp	Leu 315
Gly	Leu	Glu	Lys	Ile 320	Tyr	Ser	Ile	Val	Lys 325	Gln	Ser	Asn	Tyr	Val 330
Leu	Arg	Ile	Glu	Leu 335	Glu	Asp	Trp	Lys	Asp 340	Asn	Lys	His	Tyr	Ile 345
Glu	Tyr	Ser	Phe	Tyr 350	Leu	Gly	Asn	His	Glu 355	Thr	Asn	Tyr	Thr	Leu 360
His	Leu	Val	Ala	Ile 365	Thr	Gly	Asn	Val	Pro 370	Asn	Ala	Ile	Pro	Glu 375
Asn	Lys	Asp	Leu	Val 380	Phe	Ser	Thr	Trp	Asp 385	His	Lys	Ala	Lys	Gly 390
His	Phe	Asn	Cys	Pro 395	Glu	Gly	Tyr	Ser	Gly 400	Gly	Trp	Trp	Trp	His 405
Asp	Glu	Cys	Gly	Glu 410	Asn	Asn	Leu	Asn	Gly 415	Lys	Tyr	Asn	Lys	Pro 420
Arg	Ala	Lys	Ser	Lys 425	Pro	Glu	Arg	Arg	Arg 430	Gly	Leu	Ser	Trp	Lys 435
Ser	Gln	Asn	Gly	Arg 440	Leu	Tyr	Ser	Ile	Lys 445	Ser	Thr	Lys	Met	Leu 450
Ile	His	Pro	Thr	Asp 455	Ser	Glu	Ser	Phe	Glu 460					

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GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250  
GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300  
CCGGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350  
GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400  
CAGGCTGCCC CGCTGACGGC CAGGGTGAAG CATGTGAGGA GCCGCCCCGG 450  
AGCCAAGCAG GAGGGAAGAG GCTTTCATAG ATTCTATTCA CAAAGAATAA 500  
CCACCATTTT GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550  
TCGGACTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTTT 600  
GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTTACC TAAACAGGTA 650  
CAAGCGGGCG GGCGAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700  
CCCAGCAGCG GGTCACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750  
GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTCAACAA 800  
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CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950  
GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAACA 1000  
GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050  
GACCTGGAGC ACAAGTACCA GCACCTGGCC AACTGGCCC ACAACCAATC 1100  
AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150  
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CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250  
TGACCAGAAC CTGAAGGTGC TGCCACCCCC TCTGCCCCACT ATGCCCCACTC 1300  
TCACCAGCCT CCCATCTTCC ACCGACAAGC CGTCGGGCCC ATGGAGAGAC 1350  
TGCCCTGCAGG CCCTGGAGGA TGGCCACGAC ACCAGCTCCA TCTACCTGGT 1400  
GAAGCCGGAG AACACCAACC GCCTCATGCA GGTGTGGTGC GACCAGAGAC 1450

ACGACCCCGG	GGGCTGGACC	GTCCATCCAGA	GACGCCTGGA	TGGCTCTGTT	1500
AACTTCCTTCA	GGAAC TGGGA	GACGTACAAG	CAAGGGTTTG	GGAACATTGA	1550
CGGCGAATAC	TGGCTGGGCC	TGGAGAACAT	TTACTGGCTG	ACGAACCAAG	1600
GCAACTACAA	ACTCCTGGTG	ACCATGGAGG	ACTGGTCCGG	CCGCAAAGTC	1650
TTTGCAGAAT	ACGCCAGTTT	CCGCCTGGAA	CCTGAGAGCG	AGTATTATAA	1700
GCTGCGGCTG	GGGCGCTACC	ATGGCAATGC	GGGTGACTCC	TTTACATGGC	1750
ACAACGGCAA	GCAGTTCACC	ACCCTGGACA	GAGATCATGA	TGCTCTACACA	1800
GGAAACTGTG	CCCACTACCA	GAAGGGAGGC	TGGTGGTATA	ACGCCTGTGC	1850
CCACTCCAAC	CTCAACGGGG	TCTGGTACCG	CGGGGGCCAT	TACCGGAGCC	1900
GCTACCAGGA	CGGAGTCTAC	TGGGCTGAGT	TCCGAGGAGG	CTCTTACTCA	1950
CTCAAGAAAG	TGGTGATGAT	GATCCGACCG	AACCCCAACA	CCTTCCACTA	2000
AGCCAGCTCC	CCCTCCTGAC	CTCTCGTGGC	CATTGCCAGG	AGCCCACCCT	2050
GGTCACGCTG	GCCACAGCAC	AAAGAACAAC	TCCTCACCAG	TTCATCCTGA	2100
GGCTGGGAGG	ACCGGGATGC	TGGATTCTGT	TTTCCGAAGT	CACTGCAGCG	2150
GATGATGGAA	CTGAATCGAT	ACGGTGTTTT	CTGTCCCTCC	TACTTTTCCTT	2200
CACACCAGAC	AGCCCCTCAT	GTCTCCAGGA	CAGGACAGGA	CTACAGACAA	2250
CTCTTTCTTT	AAATAAATTA	AGTCTCTACA	ATAAAAAAAAA	2290	

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr	20	25	30	
Glu	Glu	Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys	35	40	45	
Arg	Ala	Gly	Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val	50	55	60	
Pro	Gln	Gln	Arg	Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu	65	70	75	
Pro	Glu	Val	Leu	Leu	Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu	80	85	90	
Leu	Leu	Asn	Asn	Glu	Leu	Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr	95	100	105	
Leu	Gln	Gln	Leu	Val	Glu	Val	Asp	Gly	Gly	Ile	Val	Ser	Glu	Val	110	115	120	
Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	125	130	135	
Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp	140	145	150	
Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn	Arg	Ile	Leu	Asn	Gln	155	160	165	
Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr	Lys	Asp	Leu	Glu	170	175	180	
His	Lys	Tyr	Gln	His	Leu	Ala	Thr	Leu	Ala	His	Asn	Gln	Ser	Glu	185	190	195	
Ile	Ile	Ala	Gln	Leu	Glu	Glu	His	Cys	Gln	Arg	Val	Pro	Ser	Ala	200	205	210	
Arg	Pro	Val	Pro	Gln	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Arg	Val	Tyr	215	220	225	
Gln	Pro	Pro	Thr	Tyr	Asn	Arg	Ile	Ile	Asn	Gln	Ile	Ser	Thr	Asn	230	235	240	
Glu	Ile	Gln	Ser	Asp	Gln	Asn	Leu	Lys	Val	Leu	Pro	Pro	Pro	Leu	245	250	255	
Pro	Thr	Met	Pro	Thr	Leu	Thr	Ser	Leu	Pro	Ser	Ser	Thr	Asp	Lys	260	265	270	
Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly	275	280	285	

His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn
				290					295					300
Arg	Leu	Met	Gln	Val	Trp	Cys	Asp	Gln	Arg	His	Asp	Pro	Gly	Gly
				305					310					315
Trp	Thr	Val	Ile	Gln	Arg	Arg	Leu	Asp	Gly	Ser	Val	Asn	Phe	Phe
				320					325					330
Arg	Asn	Trp	Glu	Thr	Tyr	Lys	Gln	Gly	Phe	Gly	Asn	Ile	Asp	Gly
				335					340					345
Glu	Tyr	Trp	Leu	Gly	Leu	Glu	Asn	Ile	Tyr	Trp	Leu	Thr	Asn	Gln
				350					355					360
Gly	Asn	Tyr	Lys	Leu	Leu	Val	Thr	Met	Glu	Asp	Trp	Ser	Gly	Arg
				365					370					375
Lys	Val	Phe	Ala	Glu	Tyr	Ala	Ser	Phe	Arg	Leu	Glu	Pro	Glu	Ser
				380					385					390
Glu	Tyr	Tyr	Lys	Leu	Arg	Leu	Gly	Arg	Tyr	His	Gly	Asn	Ala	Gly
				395					400					405
Asp	Ser	Phe	Thr	Trp	His	Asn	Gly	Lys	Gln	Phe	Thr	Thr	Leu	Asp
				410					415					420
Arg	Asp	His	Asp	Val	Tyr	Thr	Gly	Asn	Cys	Ala	His	Tyr	Gln	Lys
				425					430					435
Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His	Ser	Asn	Leu	Asn	Gly
				440					445					450
Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Arg	Tyr	Gln	Asp	Gly
				455					460					465
Val	Tyr	Trp	Ala	Glu	Phe	Arg	Gly	Gly	Ser	Tyr	Ser	Leu	Lys	Lys
				470					475					480
Val	Val	Met	Met	Ile	Arg	Pro	Asn	Pro	Asn	Thr	Phe	His		
				485					490			493		



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AGACACAAAA	AGCTGGCAAT	ATAGCAACTA	TGAAGAGAAA	AGCTACTAAT	350
AAAATTAACC	CAACGCATAG	AAGACTTTTT	TTTCTCTTCT	AAAAACAAC	400
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GAAGACTTTT	ACCTGGACCC	TAGGTGTGCT	ATTCTTCCTA	CTAGTGGACA	500
CTGGACATTG	CAGAGGTGGA	CAATTCAAAA	TTAAAAAAT	AAACCAGAGA	550
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ACCACCTGAT	CTGGCAACTT	CTCCCACCAA	AAGCCCTTTC	AAGATACCAC	1250
CGGTAAC TTT	CATCAATGAA	GGACCATTCA	AAGACTGTCA	GCAAGCAAAA	1300
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GTAACGCTTA	GTCTCACAGT	GTCTTTAACT	CATCTTTGCA	ATCAACAAC	3050
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CTTAGAGGTG	ACCTTGCCTT	AATATATTTG	TGAAGTTAAA	ATTTTAAAGA	3150
TAGCTCATGA	AACTTTTGCT	TAAGCAAAAA	GAAAACCTCG	AATTGAAATG	3200
TGTGAGGCAA	ACTATGCATG	GGAATAGCTT	AATGTGAAGA	TAATCATTTG	3250
GACAACTCAA	ATCCATCAAC	ATGACCAATG	TTTTTTCATCT	GCCACATCTC	3300
AAAATAAAAC	TTCTGGTGAA	ACAAATTAAA	CAAAATATCC	AAACCTCAAA	3350
AAAAA	3355				

Met 1	Lys	Thr	Phe	Thr 5	Trp	Thr	Leu	Gly	Val 10	Leu	Phe	Phe	Leu	Leu 15
Val	Asp	Thr	Gly	His 20	Cys	Arg	Gly	Gly	Gln 25	Phe	Lys	Ile	Lys	Lys 30
Ile	Asn	Gln	Arg	Arg 35	Tyr	Pro	Arg	Ala	Thr 40	Asp	Gly	Lys	Glu	Glu 45
Ala	Lys	Lys	Cys	Ala 50	Tyr	Thr	Phe	Leu	Val 55	Pro	Glu	Gln	Arg	Ile 60
Thr	Gly	Pro	Ile	Cys 65	Val	Asn	Thr	Lys	Gly 70	Gln	Asp	Ala	Ser	Thr 75
Ile	Lys	Asp	Met	Ile 80	Thr	Arg	Met	Asp	Leu 85	Glu	Asn	Leu	Lys	Asp 90
Val	Leu	Ser	Arg	Gln 95	Lys	Arg	Glu	Ile	Asp 100	Val	Leu	Gln	Leu	Val 105
Val	Asp	Val	Asp	Gly 110	Asn	Ile	Val	Asn	Glu 115	Val	Lys	Leu	Leu	Arg 120
Lys	Glu	Ser	Arg	Asn 125	Met	Asn	Ser	Arg	Val 130	Thr	Gln	Leu	Tyr	Met 135
Gln	Leu	Leu	His	Glu 140	Ile	Ile	Arg	Lys	Arg 145	Asp	Asn	Ser	Leu	Glu 150
Leu	Ser	Gln	Leu	Glu 155	Asn	Lys	Ile	Leu	Asn 160	Val	Thr	Thr	Glu	Met 165
Leu	Lys	Met	Ala	Thr 170	Arg	Tyr	Arg	Glu	Leu 175	Glu	Val	Lys	Tyr	Ala 180
Ser	Leu	Thr	Asp	Leu 185	Val	Asn	Asn	Gln	Ser 190	Val	Met	Ile	Thr	Leu 195
Leu	Glu	Glu	Gln	Cys 200	Leu	Arg	Ile	Phe	Ser 205	Arg	Gln	Asp	Thr	His 210
Val	Ser	Pro	Pro	Leu 215	Val	Gln	Val	Val	Pro 220	Gln	His	Ile	Pro	Asn 225
Ser	Gln	Gln	Tyr	Thr 230	Pro	Gly	Leu	Leu	Gly 235	Gly	Asn	Glu	Ile	Gln 240
Arg	Asp	Pro	Gly	Tyr 245	Pro	Arg	Asp	Leu	Met 250	Pro	Pro	Pro	Asp	Leu 255
Ala	Thr	Ser	Pro	Thr 260	Lys	Ser	Pro	Phe	Lys 265	Ile	Pro	Pro	Val	Thr 270
Phe	Ile	Asn	Glu	Gly 275	Pro	Phe	Lys	Asp	Cys 280	Gln	Gln	Ala	Lys	Glu 285

Ala Gly His Ser	Val	Ser Gly Ile Tyr	Met	Ile Lys Pro Glu	Asn
	290		295		300
Ser Asn Gly Pro	Met	Gln Leu Trp Cys	Glu	Asn Ser Leu Asp	Pro
	305		310		315
Gly Gly Trp Thr	Val	Ile Gln Lys Arg	Thr	Asp Gly Ser Val	Asn
	320		325		330
Phe Phe Arg Asn	Trp	Glu Asn Tyr Lys	Lys	Gly Phe Gly Asn	Ile
	335		340		345
Asp Gly Glu Tyr	Trp	Leu Gly Leu Glu	Asn	Ile Tyr Met Leu	Ser
	350		355		360
Asn Gln Asp Asn	Tyr	Lys Leu Leu Ile	Glu	Leu Glu Asp Trp	Ser
	365		370		375
Asp Lys Lys Val	Tyr	Ala Glu Tyr Ser	Ser	Phe Arg Leu Glu	Pro
	380		385		390
Glu Ser Glu Phe	Tyr	Arg Leu Arg Leu	Gly	Thr Tyr Gln Gly	Asn
	395		400		405
Ala Gly Asp Ser	Met	Met Trp His Asn	Gly	Lys Gln Phe Thr	Thr
	410		415		420
Leu Asp Arg Asp	Lys	Asp Met Tyr Ala	Gly	Asn Cys Ala His	Phe
	425		430		435
His Lys Gly Gly	Trp	Trp Tyr Asn Ala	Cys	Ala His Ser Asn	Leu
	440		445		450
Asn Gly Val Trp	Tyr	Arg Gly Gly His	Tyr	Arg Ser Lys His	Gln
	455		460		465
Asp Gly Ile Phe	Trp	Ala Glu Tyr Arg	Gly	Gly Ser Tyr Ser	Leu
	470		475		480
Arg Ala Val Gln	Met	Met Ile Lys Pro	Ile	Asp	
	485		490	491	

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TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100  
TGGGAAGGTC CGCCGCGATG GGAAGCCCT GGCTGCGTGC GCTACAGCTG 150  
CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200  
CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250  
GCGGCCCCGC ATCCACGCGG GCGACGCCCC AGGCCGCCAA CGCCAGCGAG 300  
CTGGCGGGCGC TGCATGCG CGTCGGCCGC CACGAGGAGC TGTACGCGA 350  
GCTGCAGAGG CTGGCGGCGG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400  
CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450  
GCGCAGCTGC AGCACGAGGC GGGGCCCGGG GCGGGCCCGG GGGCGGATCT 500  
GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550  
ACGCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600  
GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650  
CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700  
TCCTGCCGCC ACCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750  
AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800  
AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850  
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GAGGCCCGCC AGGCAGGCCA TGAACAGAGT GGAGTGTATG AACTGCGAGT 950  
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GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150  
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GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGCGGCTTGG 1250  
CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300  
CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350  
CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400  
CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450

[illegible]

Met	Gly	Lys	Pro	Trp	Leu	Arg	Ala	Leu	Gln	Leu	Leu	Leu	Leu	Leu	15
1				5					10						
Gly	Ala	Ser	Trp	Ala	Arg	Ala	Gly	Ala	Pro	Arg	Cys	Thr	Tyr	Thr	30
				20					25						
Phe	Val	Leu	Pro	Pro	Gln	Lys	Phe	Thr	Gly	Ala	Val	Cys	Trp	Ser	45
				35					40						
Gly	Pro	Ala	Ser	Thr	Arg	Ala	Thr	Pro	Glu	Ala	Ala	Asn	Ala	Ser	60
				50					55						
Glu	Leu	Ala	Ala	Leu	Arg	Met	Arg	Val	Gly	Arg	His	Glu	Glu	Leu	75
				65					70						
Leu	Arg	Glu	Leu	Gln	Arg	Leu	Ala	Ala	Ala	Asp	Gly	Ala	Val	Ala	90
				80					85						
Gly	Glu	Val	Arg	Ala	Leu	Arg	Lys	Glu	Ser	Arg	Gly	Leu	Ser	Ala	105
				95					100						
Arg	Leu	Gly	Gln	Leu	Arg	Ala	Gln	Leu	Gln	His	Glu	Ala	Gly	Pro	120
				110					115						
Gly	Ala	Gly	Pro	Gly	Ala	Asp	Leu	Gly	Ala	Glu	Pro	Ala	Ala	Ala	135
				125					130						
Leu	Ala	Leu	Leu	Gly	Glu	Arg	Val	Leu	Asn	Ala	Ser	Ala	Glu	Ala	150
				140					145						
Gln	Arg	Ala	Ala	Ala	Arg	Phe	His	Gln	Leu	Asp	Val	Lys	Phe	Arg	165
				155					160						
Glu	Leu	Ala	Gln	Leu	Val	Thr	Gln	Gln	Ser	Ser	Leu	Ile	Ala	Arg	180
				170					175						
Leu	Glu	Arg	Leu	Cys	Pro	Gly	Gly	Ala	Gly	Gly	Gln	Gln	Gln	Val	195
				185					190						
Leu	Pro	Pro	Pro	Pro	Leu	Val	Pro	Val	Val	Pro	Val	Arg	Leu	Val	210
				200					205						
Gly	Ser	Thr	Ser	Asp	Thr	Ser	Arg	Met	Leu	Asp	Pro	Ala	Pro	Glu	225
				215					220						
Pro	Gln	Arg	Asp	Gln	Thr	Gln	Arg	Gln	Gln	Glu	Pro	Met	Ala	Ser	240
				230					235						
Pro	Met	Pro	Ala	Gly	His	Pro	Ala	Val	Pro	Thr	Lys	Pro	Val	Gly	255
				245					250						
Pro	Trp	Gln	Asp	Cys	Ala	Glu	Ala	Arg	Gln	Ala	Gly	His	Glu	Gln	270
				260					265						
Ser	Gly	Val	Tyr	Glu	Leu	Arg	Val	Gly	Arg	His	Val	Val	Ser	Val	285
				275					280						



Trp	Cys	Glu	Gln	Gln	Leu	Glu	Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	
				290					295					300	
Arg	Arg	Gln	Asp	Gly	Ser	Val	Asn	Phe	Phe	Thr	Thr	Trp	Gln	His	
				305					310					315	
Tyr	Lys	Ala	Gly	Phe	Gly	Arg	Pro	Asp	Gly	Glu	Tyr	Trp	Leu	Gly	
				320					325					330	
Leu	Glu	Pro	Val	Tyr	Gln	Leu	Thr	Ser	Arg	Gly	Asp	His	Glu	Leu	
				335					340					345	
Leu	Val	Leu	Leu	Glu	Asp	Trp	Gly	Gly	Arg	Gly	Ala	Arg	Ala	His	
				350					355					360	
Tyr	Asp	Gly	Phe	Ser	Leu	Glu	Pro	Glu	Ser	Asp	His	Tyr	Arg	Leu	
				365					370					375	
Arg	Leu	Gly	Gln	Tyr	His	Gly	Asp	Ala	Gly	Asp	Ser	Leu	Ser	Trp	
				380					385					390	
His	Asn	Asp	Lys	Pro	Phe	Ser	Thr	Val	Asp	Arg	Asp	Arg	Asp	Ser	
				395					400					405	
Tyr	Ser	Gly	Asn	Cys	Ala	Leu	Tyr	Gln	Arg	Gly	Gly	Trp	Trp	Tyr	
				410					415					420	
His	Ala	Cys	Ala	His	Ser	Asn	Leu	Asn	Gly	Val	Trp	His	His	Gly	
				425					430					435	
Gly	His	Tyr	Arg	Ser	Arg	Tyr	Gln	Asp	Gly	Val	Tyr	Trp	Ala	Glu	
				440					445					450	
Phe	Arg	Gly	Gly	Ala	Tyr	Ser	Leu	Arg	Lys	Ala	Ala	Met	Leu	Ile	
				455					460					465	
Arg	Pro	Leu	Lys	Leu											
				470											



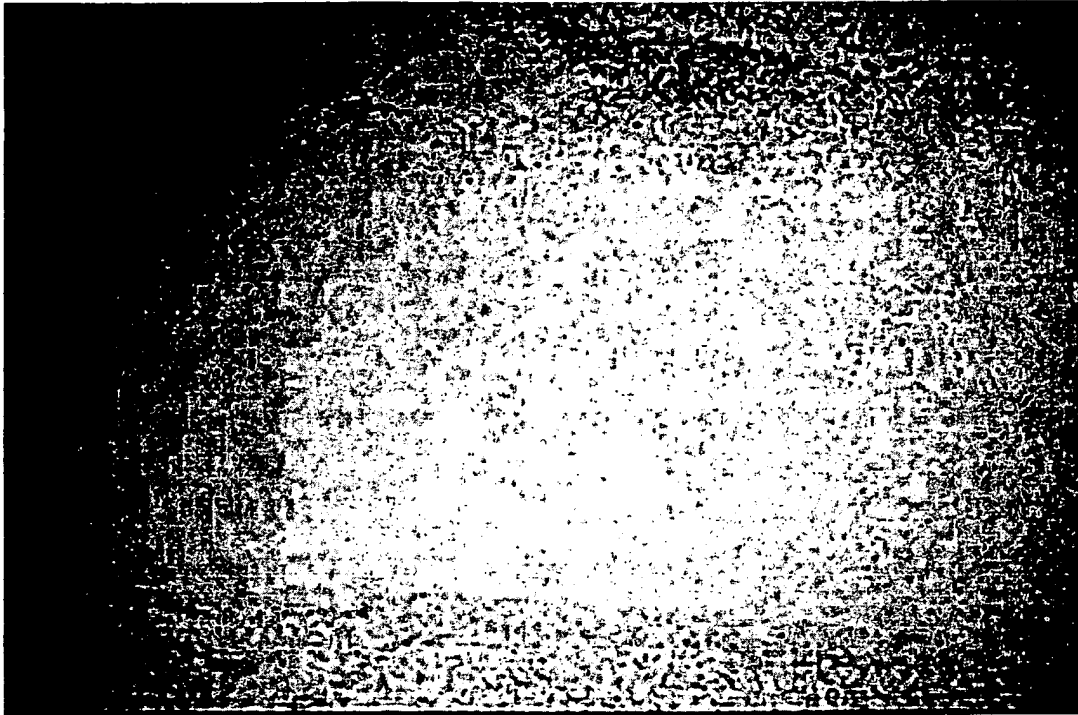
[illegible]

Figure 8-B

**THE** **NEW** **YORK** **PUBLIC** **LIBRARY**

**ASTOR LENOX TILDEN FOUNDATION**

**100 N. YERGES ST.**

**NEW YORK 17, N.Y.**

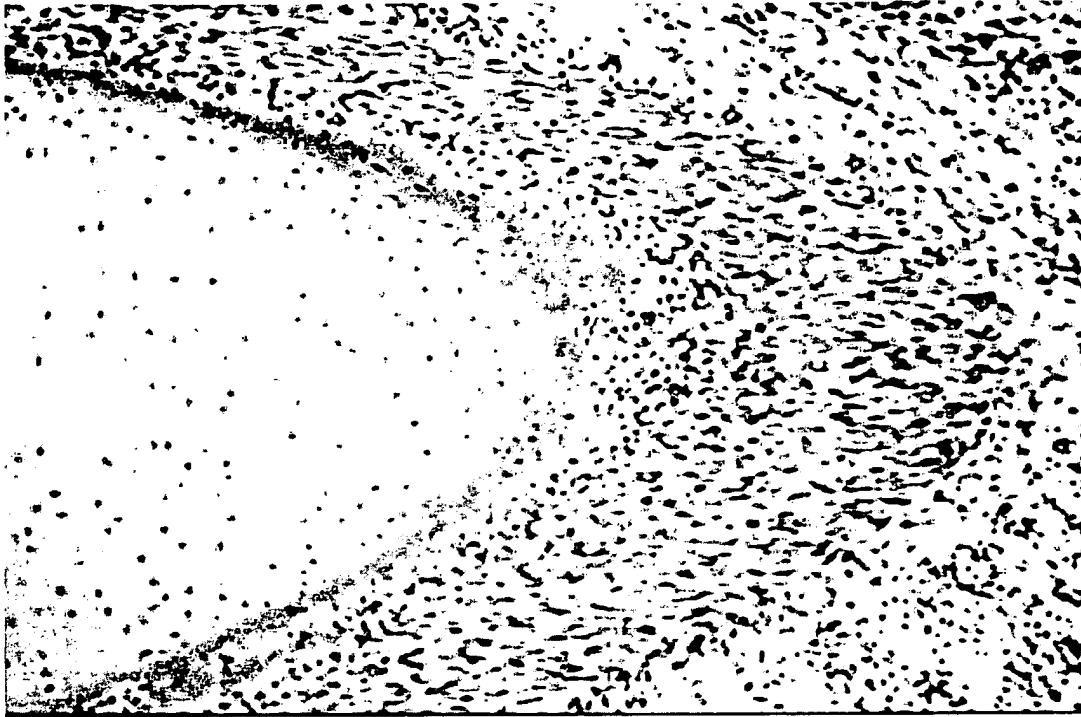


Figure 9A

# DNA 28497 Dark Field

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The white spots represent the silver grains.

---

Figure 9B

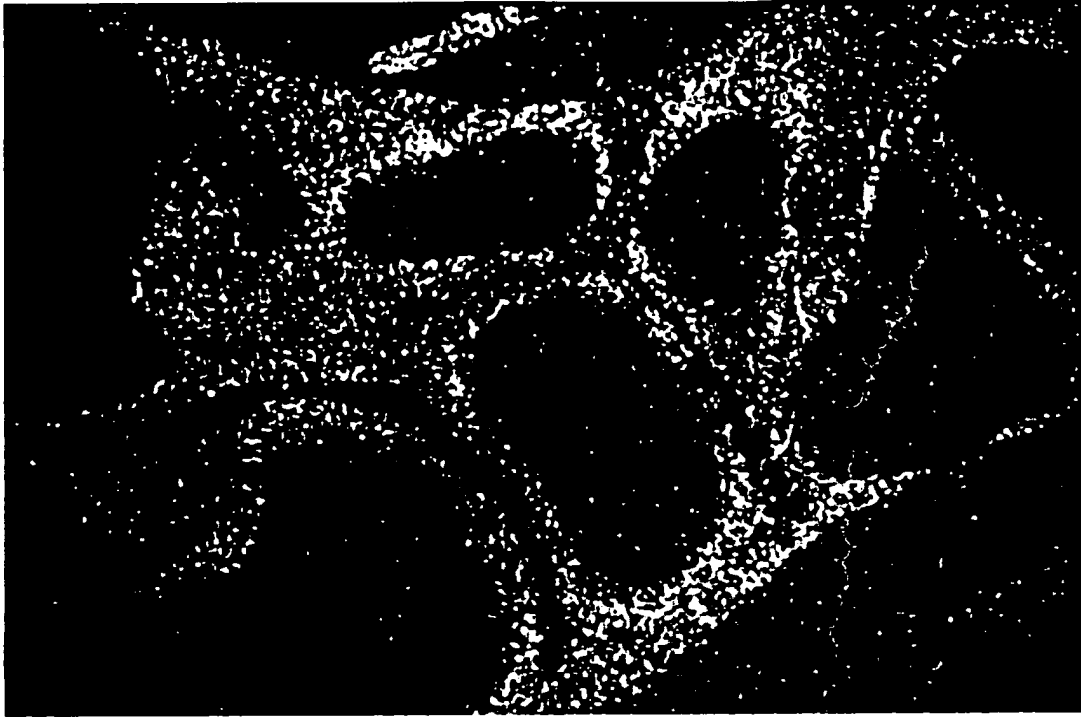
00000001.001007

[illegible]

Figure 10-A

# DNA 23339 Dark Field

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The white spots represent the silver grains.

---

Figure 10-B

00033221 001007  
200100 122200

# NL1 Northern

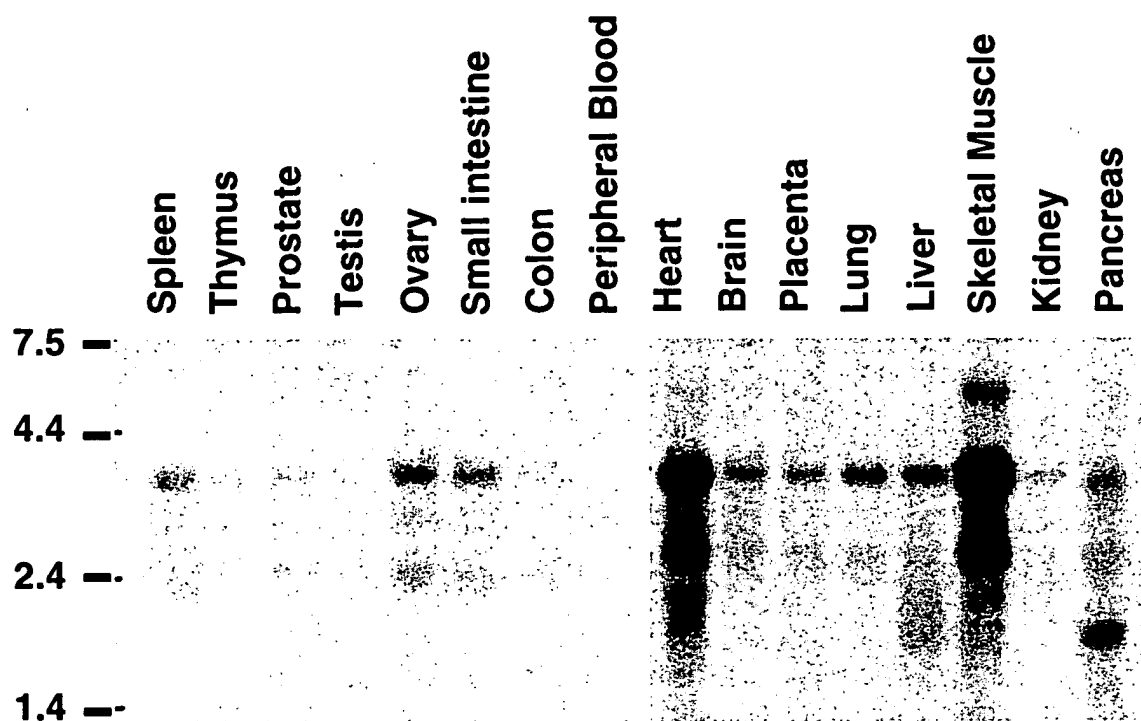


Figure 11



# NL5 Northern

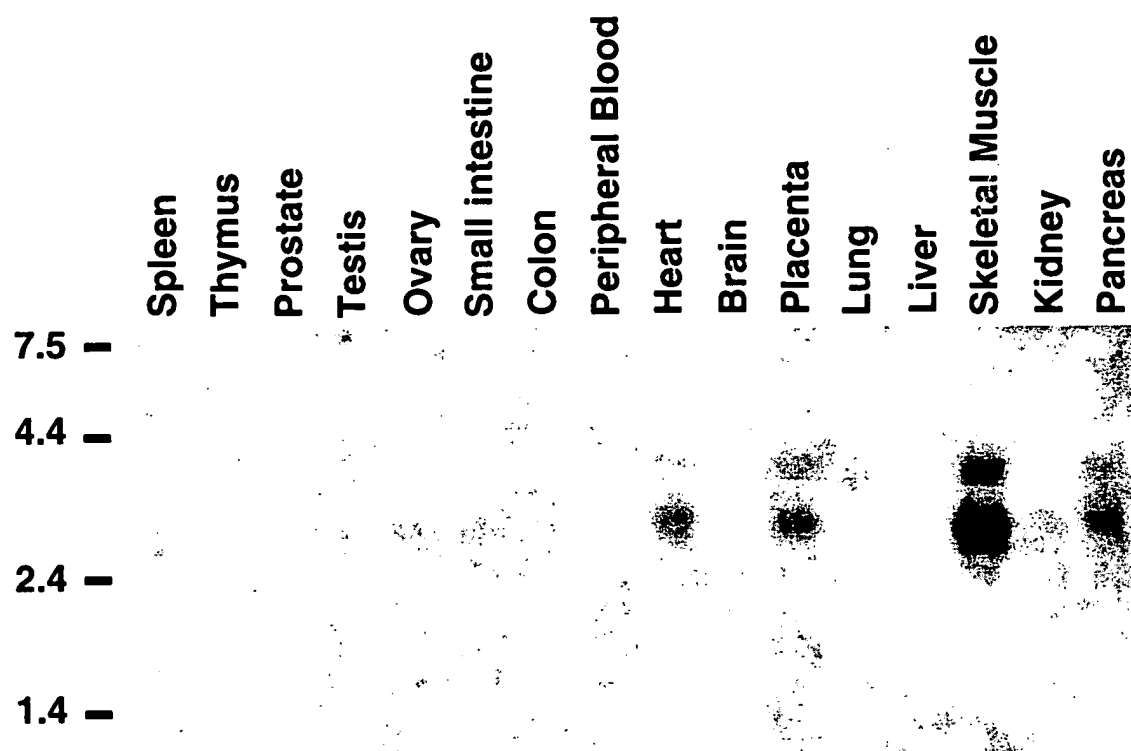


Figure 12